<110> Boronat, Albert;
Campos, Narciso;
Rodriguez-Concepcion, Manuel;
Rohmer, Michel;
Seeman, Myriam;
Valentin, Henry E.;
Venkatesh, Tyamagondlu V.;
Venkatramesh, Mylavarapu

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gct gat att cat ttt gcc ccg aca gtt gct tta aga gtg gct gaa tgc     7410
Ala Asp Ile His Phe Ala Pro Thr Val Ala Leu Arg Val Ala Glu Cys
75                  80                  85                  90

ttt gac aaa att cgt gtc aac cca ggg aat ttt g gtgagtgaaa           7454
Phe Asp Lys Ile Arg Val Asn Pro Gly Asn Phe
                95                  100

taatgatgtg tatcatttta gtgtcaatat cttatcaact ctgtgcatat gctgagaact  7514

ctacttgcag  ct gat cgc cgt gcc caa ttt gag cag ctt gaa tat act      7562
           Ala Asp Arg Arg Ala Gln Phe Glu Gln Leu Glu Tyr Thr
                       105                 110

gaa gat gat tat caa aaa gag ctt gag cat atc gag aag gtt cca aat     7610
Glu Asp Asp Tyr Gln Lys Glu Leu Glu His Ile Glu Lys Val Pro Asn
115                 120                 125                 130

atc tca ctc ttt agt gtt aat tta gtcagtaaga atgtgcagta tgtttcctta    7664
Ile Ser Leu Phe Ser Val Asn Leu
                135

cttgcatagc cacttccata tcatttcag gtc ttc tcc ccg ttg gtt gag aaa     7717
                                Val Phe Ser Pro Leu Val Glu Lys
                                    140                 145

tgc aag cag tat gga aga gca atg cgt ata gga aca aat cat gga agt     7765
Cys Lys Gln Tyr Gly Arg Ala Met Arg Ile Gly Thr Asn His Gly Ser
            150                 155                 160

ctg tct gac cgc ata atg agt tac tat ggt gat tct cca cgc gga atg     7813
Leu Ser Asp Arg Ile Met Ser Tyr Tyr Gly Asp Ser Pro Arg Gly Met
        165                 170                 175

gtattatttc ctttctgggg atttcattca aataactttt cgtttcatgg atgtcttcaa   7873

ttaatgatcg ttttgataga tgaatgacat gttctacaaa taatttcag gtt gag tct   7931
                                                    Val Glu Ser
                                                        180

gct ttg gaa ttt gcc agg atc tgt cgg aag ctg gac ttc cat aac ttt     7979
Ala Leu Glu Phe Ala Arg Ile Cys Arg Lys Leu Asp Phe His Asn Phe
            185                 190                 195

gtg ttt tca atg aaa gca agt aac cct gtt atc atg gtc caa gca tat     8027
Val Phe Ser Met Lys Ala Ser Asn Pro Val Ile Met Val Gln Ala Tyr
        200                 205                 210

cgc ttg ctt gta gca gaa atg tat aac cta ggg tgg gat tat cct ttg     8075
Arg Leu Leu Val Ala Glu Met Tyr Asn Leu Gly Trp Asp Tyr Pro Leu
    215                 220                 225

cac ttg gga gtt aca gaa gct gga gag ggt gaa gat ggg agg atg aag     8123
His Leu Gly Val Thr Glu Ala Gly Glu Gly Glu Asp Gly Arg Met Lys
230                 235                 240                 245
```

```
tct gcc att ggc att gga aca ctt ctg atg gtaattgcat ttttactttg       8173
Ser Ala Ile Gly Ile Gly Thr Leu Leu Met
                250                 255

tgtattatat tgcatatatc atatctttcc atctgcaaag ggtaagcatg ccttatgtct   8233

tccttttgtt gtcttacag gat ggc ttg ggc gat aca atc cgt gtc tcc ctc     8285
                     Asp Gly Leu Gly Asp Thr Ile Arg Val Ser Leu
                                    260                 265

acg gaa cca cct gaa gaa gag att gat cct tgc cgg aga ttg gca aat      8333
Thr Glu Pro Pro Glu Glu Glu Ile Asp Pro Cys Arg Arg Leu Ala Asn
            270                 275                 280

ctt ggc aca cat gcc gca gac ctt caa ata gga gtg gtaacgattt          8379
Leu Gly Thr His Ala Ala Asp Leu Gln Ile Gly Val
        285                 290

attacctttc tctagtttta cacttttctc ttgtttagct gccaatgcca cacattaatt   8439

ttgactattt ttagtagtgt tttgttctat ttgttctttt aagaatttct atttatatac   8499

attatatgtt ctcag gct cct ttt gaa gaa aag cac agg cgc tat ttt gat     8550
               Ala Pro Phe Glu Glu Lys His Arg Arg Tyr Phe Asp
               295                 300                 305

ttc cag cgt aga agt ggt cag ttg cct tta caa aag gag gttagttcaa      8599
Phe Gln Arg Arg Ser Gly Gln Leu Pro Leu Gln Lys Glu
            310                 315

aataactcct atagtccata gttatcataa aaacaatagt gctagatttc ttattagttg   8659

cacttatgac agggtgagga agtagactac agaggggtct tgcaccgtga tggctctgtt   8719

ttgatgtcag tttccttgga tcagttgaag gtaactcaca tatttgttac ccttttgtgc   8779

aatgtgttga tcttgtgtaa ctttaccaaa atatatttca agacaatagt ctattttgta   8839

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tcatagtaca tagtgagaat agcaatagca aaaagaaggc attgattttt ttctatctga   8959

atcaaatcaa ttgatgcatt ttgtaatgat ggaaggctct cttatttttc ag gct cct   9017
                                                          Ala Pro
                                                          320

gag ctc ctt tat agg tct ctt gct gca aag ctt gtg gtt ggc atg cct     9065
Glu Leu Leu Tyr Arg Ser Leu Ala Ala Lys Leu Val Val Gly Met Pro
            325                 330                 335

ttc aag gtctgatcct tatagctgta cattctagca aacaactaaa ctttattggt      9121
Phe Lys

acttcagtct aaactgatgt taatttttct atgaatatca g gat ctg gca act gta   9177
                                             Asp Leu Ala Thr Val
                                             340
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```
gat tct att ctt ttg aag gag ctc cca cct gta gaa gat gct caa gct     9225
Asp Ser Ile Leu Leu Lys Glu Leu Pro Pro Val Glu Asp Ala Gln Ala
345                 350                 355                 360

gtgagttcct tcaacattat ttgttctttt cacaaatcac aagcttatat taacattcta   9285

ttcctttaaa atttttgtgt tgaaatctgt aaaatggtac ag agg ctt gca ctc      9339
                                              Arg Leu Ala Leu

aaa aga tta gtt gac atc agc atg ggt gtg ttg act ccc tta tca gag     9387
Lys Arg Leu Val Asp Ile Ser Met Gly Val Leu Thr Pro Leu Ser Glu
365                 370                 375                 380

caa ctg aca aag cca ctc cca cat gca att gct ctt gtc aat gtg gat     9435
Gln Leu Thr Lys Pro Leu Pro His Ala Ile Ala Leu Val Asn Val Asp
                385                 390                 395

gaa ctg tca agc ggt gca cac aaa ctt ttg cca gaa g gtagacattt       9482
Glu Leu Ser Ser Gly Ala His Lys Leu Leu Pro Glu
            400                 405

gaatttgata atgatctttg ttgttttgtg aattgtgttt atgtcatttt ctgtatttta   9542

acattttgct tagtctgttt tattgatgaa tctttttttt atgtag  gc act aga      9596
                                                  Gly Thr Arg
                                                      410

ttg gct gtc acc ctt cgt gga gat gaa tca tat gaa cag cta gat ctt     9644
Leu Ala Val Thr Leu Arg Gly Asp Glu Ser Tyr Glu Gln Leu Asp Leu
            415                 420                 425

ctt aag ggt gtt gat gat ata aca atg tta ctg cac agt gtt cct tat     9692
Leu Lys Gly Val Asp Asp Ile Thr Met Leu Leu His Ser Val Pro Tyr
        430                 435                 440

ggt gaa gag aag act ggc aga gta cac gct gct agg ag  gtaagtgaac      9740
Gly Glu Glu Lys Thr Gly Arg Val His Ala Ala Arg Arg
    445                 450                 455

acagtaggcc agttaatacc actccctcca ttattaccat ttgttgggat gaaccgatag   9800

tcaattctaa gttacacatt aagcatgaaa aatgaaaatg gatttgactc tgcagaaaac   9860

tgacatacag accaatgttt ccacctggtt ttccattgtt ctgtacttct ctttacctaa   9920

aattttattt tttttaataa tgttttgcag g tta ttt gag tac tta gaa acc      9972
                                  Leu Phe Glu Tyr Leu Glu Thr
                                                  460

aac ggt ttg aac ttc cct gta atc cat cac ata gaa ttc ccc aaa agc    10020
Asn Gly Leu Asn Phe Pro Val Ile His His Ile Glu Phe Pro Lys Ser
    465                 470                 475

gtg aac ag  gtactatgaa gtgcttatta agagatgcat tgaccgccca            10068
Val Asn Arg
480
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```
tccttacccc ttgaaattac tgtaccttta ttctcttgtg cttatttgag ttaaattata  10128

tgcag a gat gac ctt gtt att ggt gct ggg gca aat gtt ggt gct ctt    10176
       Asp Asp Leu Val Ile Gly Ala Gly Ala Asn Val Gly Ala Leu
              485                 490                 495

cta gtt gat ggt ctt ggt gat ggt gta ctt ctt gaa gct gct gac cag    10224
Leu Val Asp Gly Leu Gly Asp Gly Val Leu Leu Glu Ala Ala Asp Gln
           500                 505                 510

gaa ttt gag ttt ttg agg gac aca tcc ttc aac ttg tta cag ggc tgc    10272
Glu Phe Glu Phe Leu Arg Asp Thr Ser Phe Asn Leu Leu Gln Gly Cys
       515                 520                 525

agg atg cgc aac aca aaa acg gtaagctgat gaattcttct ctgttagact       10323
Arg Met Arg Asn Thr Lys Thr
    530                 535

gtagatccca tgaacaacgt caacctttaa ctcgtgagat atcatgaaga agtgcaaaat  10383

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tctgcctccc ttgttttcaa tcgcatatta gctagcctga tggctaatca tgtctacatt  10683

tgcctggcag att gct atc atg ggt tgc att gtc aat ggg cca ggg gag     10732
          Ile Ala Ile Met Gly Cys Ile Val Asn Gly Pro Gly Glu
                      540                 545

atg gcc gat gct gat ttc gga tac gtt gga ggt gct cct ggg aag atc    10780
Met Ala Asp Ala Asp Phe Gly Tyr Val Gly Gly Ala Pro Gly Lys Ile
    550                 555                 560

gac ctt tat gtt ggc aag gtaacctttt cctatacttg tggaagttga           10828
Asp Leu Tyr Val Gly Lys
565                 570

atcatatcaa atggaataat ggaaatcacg gtatatcgtt gaacatagct gcaagtcaat  10888

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atgctctttg agctgaaaca aaaacttaga gctgccattt tccttccatt aacacaagtt  11008

ctacttgttt tgggtgcag acc gtc gtg caa cgg ggc att gca atg gag ggg   11060
                  Thr Val Val Gln Arg Gly Ile Ala Met Glu Gly
                                  575                 580

gcc act gac gcc ttg att cag tta atc aag gac cat ggc cgt tgg gtg    11108
Ala Thr Asp Ala Leu Ile Gln Leu Ile Lys Asp His Gly Arg Trp Val
           585                 590                 595
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gat cct cct gtt gag gag tag gccgtagcat gtagttcata tatgtactcc       11159
Asp Pro Pro Val Glu Glu
        600

tccataaaca atgttgtagc tgaggcacat tgtattgtat ccacggagta cataaataca  11219

cgttctgtac atcagtttag aaataaagta ggaatagggg tggctgcaac tttgtaacac  11279

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gaaaaactta aagaaatccg cgtcgctcgc gccgtcgcgc gcgcgggggg cgcgtagtac 32519

ctccacacac gattctgcac ttgtactacc acgcgaacct gatgcggttt accggtcatc 32579

gattggctgc gaggcttgct gttactggtg gtggtagact ggtagtacgt tgcttgtact 32639

acctcactca tgtctggaga ttactacact tcgatctttt cctctgtttt gttaattgag 32699

atttggaggt gttactgttc gctgtgtggt taagtatatt ggtgtataac tacaagttgg 32759

tactctcaaa gggaaaaaaa ggtactgcaa attggctaat ctatgattct attctgcaca 32819

tgcatataga taagcactat aataaggaac tgaggatcgt gaaaagtggc attaattata 32879

acaggaccat gtacgactat accactggca gggatttcac ggaatcaact ataggagtag 32939

gttagttggc acttggcaag gttgattgat tcactaacgt ggggaaaaga acacacgaga 32999

tcaaaggctg tcgtgggctt aaaataaaag ggcccatctg ggatcagctc ttttaagccc 33059

acatcactag ccaggaggct aggagtccag tattgcctcg tactgggccg tcctctgaaa 33119

tttggaggcc ctgtctaaaa ttctaatcaa gccttaaact taagtgacaa aataaaaaga 33179

ggtagactat ataacagcat accattacaa cggaatagct gtcgttagca cgatactcta 33239

tatgcatcag atatggtacc aggtactata ccgacgttag catgatccga taggtatagg 33299

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atctggtgta cctagatatt atgctaacat aatcatgaca tcagctattc cattggaatg  33359

atataccggt ggtatcttcg gtaaattgtg agcatgctag gaatttaagt aaagggcctt  33419

agggttaaaa tcacacgttc ttagtcactg cactatcaag tgcatttcaa ccctaatgcc  33479

cttttatgat ctatatctgc cctcctagcc tattttggac gaggctccct cgtcctagaa  33539

gtaaatcatc gtatccataa tccaaccgat tagtagagaa aaaacatact tttcgaacgc  33599

aacagttctt gtcatcttgt gctctcaaat gttcattttc cccttactta aaggacatgg  33659

aaaacagaac agaccc                                                  33675
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<210> 3
<211> 1119
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)..(1119)

<400> 3

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atg cat aac cag gct cca att caa cgt aga aaa tca aca cgt att tac      48
Met His Asn Gln Ala Pro Ile Gln Arg Arg Lys Ser Thr Arg Ile Tyr
1               5                   10                  15

gtt ggg aat gtg ccg att ggc gat ggt gct ccc atc gcc gta cag tcc      96
Val Gly Asn Val Pro Ile Gly Asp Gly Ala Pro Ile Ala Val Gln Ser
            20                  25                  30

atg acc aat acg cgt acg aca gac gtc gaa gca acg gtc aat caa atc     144
Met Thr Asn Thr Arg Thr Thr Asp Val Glu Ala Thr Val Asn Gln Ile
        35                  40                  45

aag gcg ctg gaa cgc gtt ggc gct gat atc gtc cgt gta tcc gta ccg     192
Lys Ala Leu Glu Arg Val Gly Ala Asp Ile Val Arg Val Ser Val Pro
    50                  55                  60

acg atg gac gcg gca gaa gcg ttc aaa ctc atc aaa cag cag gtt aac     240
Thr Met Asp Ala Ala Glu Ala Phe Lys Leu Ile Lys Gln Gln Val Asn
65                  70                  75                  80

gtg ccg ctg gtg gct gac atc cac ttc gac tat cgc att gcg ctg aaa     288
Val Pro Leu Val Ala Asp Ile His Phe Asp Tyr Arg Ile Ala Leu Lys
                85                  90                  95

gta gcg gaa tac ggc gtc gat tgt ctg cgt att aac cct ggc aat atc     336
Val Ala Glu Tyr Gly Val Asp Cys Leu Arg Ile Asn Pro Gly Asn Ile
            100                 105                 110
```

```
ggt aat gaa gag cgt att cgc atg gtg gtt gac tgt gcg cgc gat aaa     384
Gly Asn Glu Glu Arg Ile Arg Met Val Val Asp Cys Ala Arg Asp Lys
        115                 120                 125

aac att ccg atc cgt att ggc gtt aac gcc gga tcg ctg gaa aaa gat     432
Asn Ile Pro Ile Arg Ile Gly Val Asn Ala Gly Ser Leu Glu Lys Asp
    130                 135                 140

ctg caa gaa aag tat ggc gaa ccg acg ccg cag gcg ttg ctg gaa tct     480
Leu Gln Glu Lys Tyr Gly Glu Pro Thr Pro Gln Ala Leu Leu Glu Ser
145                 150                 155                 160

gcc atg cgt cat gtt gat cat ctc gat cgc ctg aac ttc gat cag ttc     528
Ala Met Arg His Val Asp His Leu Asp Arg Leu Asn Phe Asp Gln Phe
                165                 170                 175

aaa gtc agc gtg aaa gcg tct gac gtc ttc ctc gct gtt gag tct tat     576
Lys Val Ser Val Lys Ala Ser Asp Val Phe Leu Ala Val Glu Ser Tyr
            180                 185                 190

cgt ttg ctg gca aaa cag atc gat cag ccg ttg cat ctg ggg atc acc     624
Arg Leu Leu Ala Lys Gln Ile Asp Gln Pro Leu His Leu Gly Ile Thr
        195                 200                 205

gaa gcc ggt ggt gcg cgc agc ggg gca gta aaa tcc gcc att ggt tta     672
Glu Ala Gly Gly Ala Arg Ser Gly Ala Val Lys Ser Ala Ile Gly Leu
    210                 215                 220

ggt ctg ctg ctg tct gaa ggc atc ggc gac acg ctg cgc gta tcg ctg     720
Gly Leu Leu Leu Ser Glu Gly Ile Gly Asp Thr Leu Arg Val Ser Leu
225                 230                 235                 240

gcg gcc gat ccg gtc gaa gag atc aaa gtc ggt ttc gat att ttg aaa     768
Ala Ala Asp Pro Val Glu Glu Ile Lys Val Gly Phe Asp Ile Leu Lys
                245                 250                 255

tcg ctg cgt atc cgt tcg cga ggg atc aac ttc atc gcc tgc ccg acc     816
Ser Leu Arg Ile Arg Ser Arg Gly Ile Asn Phe Ile Ala Cys Pro Thr
            260                 265                 270

tgt tcg cgt cag gaa ttt gat gtt atc ggt acg gtt aac gcg ctg gag     864
Cys Ser Arg Gln Glu Phe Asp Val Ile Gly Thr Val Asn Ala Leu Glu
        275                 280                 285

caa cgc ctg gaa gat atc atc act ccg atg gac gtt tcg att atc ggc     912
Gln Arg Leu Glu Asp Ile Ile Thr Pro Met Asp Val Ser Ile Ile Gly
    290                 295                 300

tgc gtg gtg aat ggc cca ggt gag gcg ctg gtt tct aca ctc ggc gtc     960
Cys Val Val Asn Gly Pro Gly Glu Ala Leu Val Ser Thr Leu Gly Val
305                 310                 315                 320

acc ggc ggc aac aag aaa agc ggc ctc tat gaa gat ggc gtg cgc aaa    1008
Thr Gly Gly Asn Lys Lys Ser Gly Leu Tyr Glu Asp Gly Val Arg Lys
                325                 330                 335
```

```
gac cgt ctg gac aac aac gat atg atc gac cag ctg gaa gca cgc att    1056
Asp Arg Leu Asp Asn Asn Asp Met Ile Asp Gln Leu Glu Ala Arg Ile
            340                 345                 350

cgt gcg aaa gcc agt cag ctg gac gaa gcg cgt cga att gac gtt cag    1104
Arg Ala Lys Ala Ser Gln Leu Asp Glu Ala Arg Arg Ile Asp Val Gln
        355                 360                 365

cag gtt gaa aaa taa                                               1119
Gln Val Glu Lys
    370
```

<210> 4
<211> 686
<212> PRT
<213> Oryza sativa

<400> 4

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Met Ala Thr Gly Val Ala Pro Ala Pro Leu Pro His Val Arg Val Arg
  1               5                  10                  15

Asp Gly Gly Ile Gly Phe Thr Arg Ser Val Asp Phe Ala Lys Ile Leu
             20                  25                  30

Ser Val Pro Ala Thr Leu Arg Val Gly Ser Ser Arg Gly Arg Val Leu
         35                  40                  45

Val Ala Lys Ser Ser Ser Thr Gly Ser Asp Thr Met Glu Leu Glu Pro
     50                  55                  60

Ser Ser Glu Gly Ser Pro Leu Leu Gly Ile Thr Arg Arg Leu Leu Phe
 65                  70                  75                  80

Thr Leu His Met Val Gly Asn Val Pro Leu Gly Ser Asp His Pro Ile
                 85                  90                  95

Arg Ile Gln Thr Met Thr Thr Ser Asp Thr Lys Asp Val Ala Lys Thr
            100                 105                 110

Val Glu Glu Val Met Arg Ile Ala Asp Lys Gly Ala Asp Phe Val Arg
        115                 120                 125

Ile Thr Val Gln Gly Arg Lys Glu Ala Asp Ala Cys Phe Glu Ile Lys
    130                 135                 140

Asn Thr Leu Val Gln Lys Asn Tyr Asn Ile Pro Leu Val Ala Asp Ile
145                 150                 155                 160

His Phe Ala Pro Thr Val Ala Leu Arg Val Ala Glu Cys Phe Asp Lys
                165                 170                 175

Ile Arg Val Asn Pro Gly Asn Phe Ala Asp Arg Arg Ala Gln Phe Glu
            180                 185                 190
```

Gln Leu Glu Tyr Thr Glu Asp Asp Tyr Gln Lys Glu Leu Glu His Ile
195 200 205

Glu Lys Val Pro Asn Ile Ser Leu Phe Ser Val Asn Leu Val Phe Ser
210 215 220

Pro Leu Val Glu Lys Cys Lys Gln Tyr Gly Arg Ala Met Arg Ile Gly
225 230 235 240

Thr Asn His Gly Ser Leu Ser Asp Arg Ile Met Ser Tyr Tyr Gly Asp
245 250 255

Ser Pro Arg Gly Met Val Glu Ser Ala Leu Glu Phe Ala Arg Ile Cys
260 265 270

Arg Lys Leu Asp Phe His Asn Phe Val Phe Ser Met Lys Ala Ser Asn
275 280 285

Pro Val Ile Met Val Gln Ala Tyr Arg Leu Leu Val Ala Glu Met Tyr
290 295 300

Asn Leu Gly Trp Asp Tyr Pro Leu His Leu Gly Val Thr Glu Ala Gly
305 310 315 320

Glu Gly Glu Asp Gly Arg Met Lys Ser Ala Ile Gly Ile Gly Thr Leu
325 330 335

Leu Met Asp Gly Leu Gly Asp Thr Ile Arg Val Ser Leu Thr Glu Pro
340 345 350

Pro Glu Glu Glu Ile Asp Pro Cys Arg Arg Leu Ala Asn Leu Gly Thr
355 360 365

His Ala Ala Asp Leu Gln Ile Gly Val Ala Pro Phe Glu Glu Lys His
370 375 380

Arg Arg Tyr Phe Asp Phe Gln Arg Arg Ser Gly Gln Leu Pro Leu Gln
385 390 395 400

Lys Glu Ala Pro Glu Leu Leu Tyr Arg Ser Leu Ala Ala Lys Leu Val
405 410 415

Val Gly Met Pro Phe Lys Asp Leu Ala Thr Val Asp Ser Ile Leu Leu
420 425 430

Lys Glu Leu Pro Pro Val Glu Asp Ala Gln Ala Arg Leu Ala Leu Lys
435 440 445

Arg Leu Val Asp Ile Ser Met Gly Val Leu Thr Pro Leu Ser Glu Gln
450 455 460

Leu Thr Lys Pro Leu Pro His Ala Ile Ala Leu Val Asn Val Asp Glu
465 470 475 480

Leu Ser Ser Gly Ala His Lys Leu Leu Pro Glu Gly Thr Arg Leu Ala
485 490 495

Val Thr Leu Arg Gly Asp Glu Ser Tyr Glu Gln Leu Asp Leu Leu Lys
500 505 510

Gly Val Asp Asp Ile Thr Met Leu Leu His Ser Val Pro Tyr Gly Glu
515 520 525

Glu Lys Thr Gly Arg Val His Ala Ala Arg Arg Leu Phe Glu Tyr Leu
530 535 540

Glu Thr Asn Gly Leu Asn Phe Pro Val Ile His His Ile Glu Phe Pro
545 550 555 560

Lys Ser Val Asn Arg Asp Asp Leu Val Ile Gly Ala Gly Ala Asn Val
565 570 575

Gly Ala Leu Leu Val Asp Gly Leu Gly Asp Gly Val Leu Leu Glu Ala
580 585 590

Ala Asp Gln Glu Phe Glu Phe Leu Arg Asp Thr Ser Phe Asn Leu Leu
595 600 605

Gln Gly Cys Arg Met Arg Asn Thr Lys Thr Ile Ala Ile Met Gly Cys
610 615 620

Ile Val Asn Gly Pro Gly Glu Met Ala Asp Ala Asp Phe Gly Tyr Val
625 630 635 640

Gly Gly Ala Pro Gly Lys Ile Asp Leu Tyr Val Gly Lys Thr Val Val
645 650 655

Gln Arg Gly Ile Ala Met Glu Gly Ala Thr Asp Ala Leu Ile Gln Leu
660 665 670

Ile Lys Asp His Gly Arg Trp Val Asp Pro Pro Val Glu Glu
675 680 685

<210> 5
<211> 594
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> unsure
<222> (1..594)
<223> unsure at all n locations

<400> 5

aaaatcgtca atccctctca aactcttctc accactaatt tcttcctctg gaacattctc 60

ttctctatta ttttgattcc cttggcctca acactggttt ctcaattgca tgatcttggc 120

tcgtcttcag ttactttgat tcactgagaa aaatggcgac tggagtattg ccagctccgg 180

tttctgggat caagataccg gattcgaaag tcgggtttgg taaaagcatg aatcttgtga 240

gaatttgtna tgttaggagt ctaagatctg ctaggagaag agtttcggtt atccggaatt 300

caaaccaagg ctctgattta gctgagcttc aaccctgcat ccgaaggaaa gcccctcttc 360

ttagtgccaa ggcaggaaat attgtgaatc attgcataan gcggttagga ggaagnctcg 420

gacctgtaat ggttgaaatg tcgncccttn gaagngnaca ccggtanggg tcaaacggtg 480

ccttcttngg gtacaaaang tnttccttgg ancctnttng tgggggtttt gggattgcgg 540

aaaaaggggc tgnttttnaa gggnacctnn caaggnagna agggngggtc tttt 594

<210> 6
<211> 615
<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (1..615)
<223> unsure at all n locations

<400> 6

accagaagtg atgagcctta tgaagaactg gacattctta agggtgttga tgctactatg 60

cttttccatg accttcctta tacagaagac agaattagca gagtgcatgc aaccagacgg 120

ttatttgagt acctatctga caattctcta aacttccctg ttattcacca tattcagttc 180

ccaaatggga ttcacaggga tgacttggta attggtgctg gttctgatgc tggagccctt 240

ctggttgatg ggcttggaga tggactactt ttggaagccc cggacaagga ttttgaattt 300

attagaaaca cttctttcaa tttgttgcaa ggctgcagaa tgagaaatac aaagacagag 360

tatgtctcat gtccatcctg tggcagaaca ttgtttgatc ttcaagaagt aagtgcacaa 420

attcgggaga agacatcaca cctncctggt gtttcgattg caatcatggg atgcattgtt 480

aatggaccag gggagatggc tgatgcagac tttgggtatg tgggaagcac tccccggaag 540

attgacctct atgttgggaa gactggtgtg aagcgtggga attcaatgga gcatgccaac 600

catggcttga tccga 615

<210> 7
<211> 589
<212> DNA
<213> Lycopersicon esculentum

<400> 7

tggcgatgaa tcacatgatg agttggaaat cctgaagagc tctgatgtta caatgattct 60

tcataatctg ccatatacag aggaaaaaat tggcagggtt caagcagcca ggaggctttt 120

tgagtatctt tccgagaatt ccttgaactt tccagtgatt catcacatac aatttcccag 180

caacacccac agagatgact tagtgattgg tgccgggaca aatgcgggag ccctcttggt 240

agatgggctt ggtgatggac ttctcttgga agctccagac aaggattttg attttctcag 300

aaatacatct ttcaatttgc ttcaaggttg cagaatgcgg aacacaaaaa cggaatatgt 360

atcatgccca tcctgtggca gaactttatt cgatcttcaa gagataagcg ctcaaattag 420

agagaagacg tcacacttgc ctggtgtttc aattgccatc atgggttgca ttgtgaatgg 480

acctggggag atggctgatg ctgactttgg atatgttggt ggtgctcctg gaaagattga 540

cctttacgtc ggcaagacag tggtgaaacg ccctattgaa atggagcat 589

<210> 8
<211> 617
<212> DNA
<213> Mesembryanthemum crystallinum

<400> 8

gaaaagcata gacattattt tgactttcaa cgtagaactg gtcaattacc gattcagaaa 60

gagggtgaag atgtggacta tagaggtgtc ctacaccgtg atggttctgt cctcatgact 120

gtttccttgg acatgttgaa gacacctgaa ctcctttaca agtcattagc agcaaagctt 180

gttgttggca tgccatttaa ggatctggct actgtagact ctatttttct gagagagctt 240

tcaccagtag atgactctga tgctcggcta gctctgaaga ggttaataga tataagtatg 300

ggtgtcatag ctccttttc tgagcaactg acaaagccct tgccaaatgc aattgtattg 360

gtgaacctta aagagttgtc aaccggtgca tacaagcttt taccagtagg aacccgcttg 420

gcagtatctg tgcgaggtga tgaaccatat tgagacattg gagatcctta aagatattga 480

tgcttcaatg gctttttatg aactgtcttt taccgagagg atattcacac agtgcatgct 540

ggaccaaagc ttttgaggtc ctatcagata agcttggacc tcccgtaatt aacatatcct 600

atcccttcgg attaagg 617

<210> 9
<211> 416
<212> DNA
<213> Oryza sativa

<220>
<221> unsure
<222> (1..416)
<223> unsure at all n locations

<400> 9

ggattcggca cgagtctaat tgatggtctt ggtgatggtg tacttcttga aagctgctga 60

ccaagaaatt tgagtttttg agggacacat cctccaactt gttacagggc tgcaggatgc 120

gcaacacaaa aacggaatat ttccctggtc ctcctggtgg gcggacacnc tttnaccncc 180

aaaaattcan tgctcaaatt aaanaaaaaa ccnctcatct gccaggcntc tctattgcta 240

tcatgggtng cattgtcaat gggccagggg aaatggccaa tcctaattnc ggatacttng 300

gaggtgccct ggagaaaatc nacctntatn ttggttnttt tttttnnaac ggggcatngc 360

aanagaaggg ggcccnnacc ccnanatncn ttcnccgggn ccngggccgn ggggtt 416

<210> 10
<211> 621
<212> DNA
<213> Zea mays

<400> 10

gaattcggca ccagaagcca ctcccacatg caattgtact tgtcaacctc gacgaattgt 60

caagtggtgc acacaaactt ttgccagaag gcactagact agctgtcact cttcgtggtg 120

atgaatcata cgagcagcta gatattctta aggatgttga tgatataaca atgttgttac 180

ataatgttcc atatggtgag gagaagacag gcagggtgca tgctgctagg aggttatttg 240

agtacttaca ggccaatggc ttgaacttcc ctgtaattca tcacataaat ttccctgaaa 300

ccattgacag agatggtctt gtcattggtg ctggggccaa cgttggtgct ctcttagtcg 360

atggtcttgg tgatggtgta ttccttgaag ctgctgacca ggaatttgag tttctgaggg 420

acacatcttt caacttgctc caaggttgca ggatgcgcaa cacaaaaact gaatatgtgt 480

cttgtccttc ctgcggccga acactctttg accttcagga aatcagcgct gagattagag 540

aaaagacctc tcatctgcca ggtgtctcga tcgctatcat gggctgtatt gcaatggacc 600

aggagagatg gctgatgccg a 621

<210> 11
<211> 601
<212> DNA
<213> Pinus taeda

<220>
<221> unsure
<222> (1..601)
<223> unsure at all n locations

<400> 11

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gtactatgag ttattatggt gattctccca ggggtatggt ggaatcagca tttgaatttg 120

cacgcatttg ccggaagttg ggttttcata attttgtgtt ttcaatgaaa gcgagcgatc 180

ctgtagtcat ggttcaggca taccgtttac ttgttgcgga gatgtatgtg caaggatggg 240

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ctgcaattgg cattggaaca cttttgcagg atggtttggg tgatactatt cgagtttccc 360

ttacagaacc tccagaagag gagatcaatc cctgtagaag acttgcaaat cttgggatgc 420

aagctgcaaa gctanggaaa ggagtggctc cttttgagga gaacatcgtc attactttac 480

tttccaacgc angactggcn agctccagta cagaaggagg gtgatgaggt ggatacagag 540

gagtccgcat cgtgatggtc tgttctaatg tcagtgtcct tgacagntga agacacanaa 600

a 601

<210> 12
<211> 443
<212> DNA
<213> Physcomitrella patens

<400> 12

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ccggtcgtaa tggttcaagc atatcggctt ttagtatctg agatgtatgt gaacaactgg 120

gactacccat tacatcttgg tgttactgag gctggagagg gagaggatgg tcgcatgaag 180

tcagctatcg gcattggtgc tttacttcag gatggtctcg gtgacaccat acgtgtttca 240

ttgacggaag ctcctgaaga agaaattgat ccttgcacaa agcttgcaaa ccttggcatg 300

aagatttctg cagaacagaa gggggtggct gaattcgaag agaagcaccg gcgatacttt 360

gacttccaac gaaggaccgg ccaacttcca ctgcagaggg agggagagtt ggtggactac 420

agaaacgttc tgcaccgtga tgg 443

<210> 13
<211> 938
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> unsure
<222> (1..938)
<223> unsure at all n locations

<400> 13

atgatactgc cagctannnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 60

nnnnnnnnnn nnnnnnnnnn nnnccacgcg tccgaaaacg ttttatcctg agtttctttc 120

accatccagc ttcatttgtg aaaaatcgtc aatccctctc aaactcttct caccactaat 180

ttcttcctct ggaacattct cttctctatt attttgattc ccttggcctc aacactggtt 240

tctcaattgc atgatcttgg ctcgtcttca gttactttga ttcactgaga aaaatggcga 300

ctggagtatt gccagctccg gtttctggga tcaagatacc ggattcgaaa gtcgggtttg 360

gtaaaagcat gaatcttgtg agaatttgtg atgttaggag tctaagatct gctaggagaa 420

gagtttcggt tatccggaat tcaaaccaag gctctgattt agctgagctt caacctgcat 480

ccgaaggaag ccctctctta gtgccaagac agaaatattg tgaatcattg cataagacgg 540

tgagaaggaa gactcgtact gttatggttg gaaatgtcgc ccttggaagc gaacatccga 600

taaggattca aacgatgact acttcggata caaaagatat tactggaact gttgatgagg 660

ttatgagaat agcggataaa ggagctgata ttgtaaggat aactgtccaa gggaagaaag 720

aggcggatgc gtgctttgaa ataaaagata aactcgttca gcttaattac aatataccgc 780

tggttgcaga tattcattgt gcccctactg tagccttacg agtcgctgaa tgctttgaca 840

agatccgtgt caacccagga aattttgcgg acaggcgggc ccagtttgag acgattgatt 900

atacagaaga tgaatatcag aaagaactcc agcatatc 938

<210> 14
<211> 432
<212> DNA
<213> Arabidopsis thaliana

<400> 14

agcataacaa ggctctgatt tagctgagct tcaacctgca tccgaaggaa gccctctctt 60

agtgccaaga cagaaatatt gtgaatcatt gcataagacg gtgagaagga agactcgtac 120

tgttatggtt ggaaatgtcg cccttggaag cgaacatccg ataaggattc aaacgatgac 180

tacttcggat acaaaagata ttactggaac tgttgatgag gttatgagaa tagcggataa 240

aggagctgat attgtaagga taactgttca agggaagaaa gaggcggatg cgtgctttga 300

aataaaagat aaactcgttc agcttaatta caatataccg ctggttgcag atattcattt 360

tgcccctact gtagccttac gagtcgctga atgctttgac aagatccgtg tcaacccaag 420

aaattttgcg ga 432

<210> 15
<211> 528
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> unsure
<222> (1..528)
<223> unsure at all n locations

<400> 15

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tccgggaatt cccngggtcg acccacgcgt ccgaaagaac tccagcatat cgagcaggtc 120

ttcactcctt tggttgagaa atgcaaaaag tacgggagag caatgcgtat tgggacaaat 180

catggaagtc tttctgaccg tatcatgagc tattacgggg attctccccg aggaatggtt 240

gaatctgcgt ttgagtttgc aagaatatgt cggaaattag actatcacaa ctttgttttc 300

tcaatgaaag cgagcaaccc agtgatcatg gtccaggcgt accgtttact tgtggctgag 360

atgtatgttc atggatggga ttatcctttg catttgggag ttactgaggc aggagaaggc 420

gaagatggac ggatgaaatc tgcgattgga attgggacgc ttcttcagga cgggctcggt 480

gacacaataa gagtttcact gacggagcca ccagaagagg agatagat 528

<210> 16
<211> 379
<212> DNA
<213> Arabidopsis thaliana

<400> 16

gcgtattggg acaaatcatg gaagtctttc tgaccgtatc atgagctatt acggggattc 60

tccccgagga atggttgaat ctgcgtttga gtttgcaaga atatgtcgga aattagacta 120

tcacaacttt gttttctcaa tgaaagcgag caacccagtg atcatggtcc aggcgtaccg 180

tttacttgtg gctgagatgt atgttcatgg atgggattat cctttgcatt tgggagttac 240

tgaggcagga gaaggcgaag atggacggat gaaatctgcg attggaattg ggacgcttct 300

tcaggacggg ctcggtgaca caataagagt ttcactgacg gagccaccag aagaggagat 360

agatccctgc aagcgattg 379

<210> 17
<211> 395
<212> DNA
<213> Arabidopsis thaliana

<400> 17

aaagaactcc agcatatcga gcaggtcttc actcctttgg ttgagaaatg caaaaagtac 60

gggagagcaa tgcgtattgg gacaaatcat ggaagtcttt ctgaccgtat catgagctat 120

tacggggatt ctccccgagg aatggttgaa tctgcgtttg agtttgcaag aatatgtcgg 180

aaattagact atcacaactt tgttttctca atgaaagcga gcaacccagt gatcatggtc 240

caggcgtacc gtttacttgt ggctgagatg tatgttcatg gatgggatta tcctttgcat 300

ttgggagtta ctgaggcagg agaaggcgaa gatggacgga tgaaatctgc gattggaatt 360

ggggacactt cttcaggacg ggctcggtga cacaa 395

<210> 18
<211> 395
<212> DNA
<213> Arabidopsis thaliana

<400> 18

aaagaactcc agcatatcga gcaggtcttc actcctttgg ttgagaaatg caaaaagtac 60

gggagagcaa tgcgtattgg gacaaatcat ggaagtcttt ctgaccgtat catgagctat 120

tacggggatt ctccccgagg aatggttgaa tctgcgtttg agtttgcaag aatatgtcgg 180

gaattagact atcacaactt tgttttctca atgaaagcga gcaacccagt gatcatggtc 240

caggcgtacc gtttacttgt ggctgagatg tatgttcatg gatgggatta tcctttgcat 300

ttgggagtta ctgatgcagg agaaggcgaa gatggacgga tgaaatctgc gattggaatt 360

gggacgcttc ttcaggacgg gctcggtgac acaat 395

<210> 19
<211> 412
<212> DNA
<213> Arabidopsis thaliana

<400> 19

atgctggagg ccttcttgtg gatggactag gtgatggcgt aatgctcgaa gcacctgacc 60

aagattttga ttttcttagg aatacttcct tcaacttatt acaaggatgc agaatgcgta 120

acactaagac ggaatatgta tcgtgcccgt cttgtggaag aacgcttttc gacttgcaag 180

aaatcagcgc cgagatccga gaaaagactt cccatttacc tggcgtttcg atcgcaatca 240

tgggatgcat tgtgaatgga ccaggagaaa tggcagatgc tgatttcgga tatgtaggtg 300

gttctcccgg aaaaatcgac ctttatgtcg gaaagacggt ggtgaagcgt gggatagcta 360

tgacggaggc aacagatgct ctgatcggtc tgatcaaaga acatggtcgt tg 412

<210> 20
<211> 1172
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> unsure
<222> (1..1172)
<223> unsure at all n locations

<400> 20

gggtatgcca ttcaaggatc tggcaactgt tgattcaatc ttattaaaga gagctaccgc 60

ctgtagatga tcaagtggct cgtttggctc taaaacggtt gattgatgtc agtatgggag 120

ttatagcacc tttatcagag caactaacaa agccattgcc caatgccatg gttcttgtca 180

acctcaagga actatctggt ggcgcttaca agcttctccc tgaaggtaca cgcttggttg 240

tctctctacg aggcgatgag ccttacgagg agcttgaaat actcaacaac attgatgcta 300

cgatgattct ccatgatgta cctttcactg aagacaaagt tagcagagta catgcagctc 360

ggaggctatt cgagttctta tccgagaatt cagttaactt tcctgttatt catcacataa 420

acttcccaac cggaatccac agagacgaat tggtgattca tgcagggaca tatgctggag 480

gccttcttgt ggatggacta cgtgatggcg taatgctcga agcacctgac caagattttg 540

attttcttag gaatacttcc ttcaacttat tacaaggatg cagaatgcgt aacactaaga 600

cggaatatgt atcgtgcccg tcttgtggaa gaacgctttt cgacttgcaa gaaatcagcg 660

ccgagatccg agaaaagact tcccatttac ctggcgtttc gatcgcaatc atgggatgca 720

ttgtgaatgg accaggagaa atggcagatg ctgatttcgg atatgtaggt ggttctcccg 780

gaaaaatcga cctttatgtc ggaaagacgg tggtgaagcg tgggatagct atgacggagg 840

caacagatgc tctgatcggt ctgatcaaag aacatggtcg ttgggtcgac ccgcccgtgg 900

ccgatgagta gatttcaaaa cggagaaaga tgggtgggcc attctttgaa aactgtgaga 960

ggagatatat atatttgtgt gtgtatatca tctgtttgtt gtgtattgca tcattcattt 1020

tggacaaatg tccaaattct cttaagttga taaaagttct taggccaaat taaatttaat 1080

ataaaaaaaa aaaaaaaaag gcnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 1140

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nn 1172

<210> 21
<211> 584
<212> DNA
<213> Zea mays

<400> 21

caggttaatt aattcctgta cgccgtcggt ttcgggtact cgtttaattt cttcccgacc 60

acggttgatg gcaatgtaac cggcttgttt acccacatag ccatagtcgg catcggccat 120

ttccccgggg ccattgacaa tacagcccat gacggcgatg tctaaacccg ttagatgttt 180

agtggcttct cggacttcat gtaacacgtc ttccaagttg aacaacgtgc ggccacagga 240

aggacaggcc acatattcca ccatggtttt ccgcaaaccc agcgcctgga gaatgctgta 300

gcaaacggga atttcttttt cgggggcttc ggtgagggat acccggatag tatcgccaat 360

gccatcagct aaaagggtgg caatgccagc ggtggattta atgcggccat attccccatc 420

cccggcttcg gtaaccccta gatggagggg ataatccatg cccaactcgt tcatacgttt 480

caccatgagg cgataggcgg ccaacattac cggtacccgg gacgctttca tggaaacgac 540

taggttgcgg aaatctaaag actcacaaat tttgatgaat tcca 584

<210> 22
<211> 670
<212> DNA
<213> Zea mays

<400> 22

caggtcgact ctagaggatc ggcgttaacc atggttctct ctccgaaaga atgcttttac 60

ctacttttta cccccgaggg catggtgcaa tcggccctgg aattcatcaa aatttgtgag 120

tccttagatt tccgcaacct agtcgtttcc atgaaagcgt cccgggtacc ggtaatgttg 180

gccgcctatc gcctcatggt gaaacgtatg gacgagttgg gcatggatta tcccctccat 240

ctaggggtta ccgaagccgg ggatggggaa tatggccgca ttaaatccac cgctggcatt 300

gccacccttt tagctgatgg cattggcgat actatccggg tatccctcac cgaagccccc 360

gaaaaagaaa ttcccgtttg ctacagcatt ctccaggcgc tgggtttgcg gaaaaccatg 420

gtggaatatg tggcctgtcc ttcctgtggc cgcacgttgt tcaacttgga agacgtgtta 480

catgaagtcc gagatgccac taaacatcta acgggtttag actttcgccg tcatgggctg 540

tattgtcaat ggccccgggg caatggccga tgccgactat ggctatgtgg gtaaacaagc 600

cggttacatt gccatcaacc gtggtcggga agaaattaaa cgagtacccg aaaccgacgg 660

cgtacaggaa 670

<210> 23
<211> 596
<212> DNA
<213> Zea mays

<220>
<221> unsure
<222> (1..596)
<223> unsure at all n locations

<400> 23

caggtcgact ctagaggatc ggcgttaacc atggttctct ctccgaaaga atgcttttac 60

ctacttttta cccccgaggg catggtgcaa tcggccctgg aattcatcaa aatttgtgag 120

tccttagatt tccgcaacct agtcgtttcc atgaaagcgt cccgggtacc ggtaatgttg 180

gccgcctatc gcctcatggt gaaacgtatg gacgagttgg gcatggatta tcccctccat 240

ctaggggtta ccgaagccgg ggatggggaa tatggccgca ttaaatccac cgctggcatt 300

gccacccttt tagctgatgg cattggcgat actatccggg tatccctcac cgaagccccc 360

gaaaaagaaa ttcccgtttg ctacagcatt ctccaggcgc tgggtttgcg gaaaaccatg 420

gtggaatatg tggcctgtcc ttcctgtggc cgcacgttgt tcaacttgga agacgtgtta 480

catgaagtcc gagatgccac taaacatcta acgtgtttag actttcgncg tcatgtgctg 540

tattgtcaat ggccccggtg caatggccga tgccgactat ggctatgtgg gtaaac 596

<210> 24
<211> 403
<212> DNA
<213> Zea mays

<400> 24

cagacaagga ggaggaaaac tcgaactgtg atggtgggga atgtgccact tgggagtgat 60

caccccataa ggattcaaac catgacgact tcagatacca aggatgttgc gaaaacagta 120

gaggaggtga tgaggatagc agataaagga gctgatcttg ttagaataac agtccagggt 180

aggaaggaag ctgatgcctg ctttgagatc aagaacactc tggttcagaa gaattacaac 240

attccactag tggccgatat tcattttgct cctacggtag ctctaaaggt ggcagaatgt 300

tttgacaaaa ttcgtgtgaa cccaggaaat tttgctgatc gtcgtgctca atttgaaaag 360

ctggaatata ctgacgacga ctaccaaaaa gagctagagc ata 403

<210> 25
<211> 293
<212> DNA
<213> Zea mays

<400> 25

cagacaaggc ggaggaaaac tcgaactgtg atggtgggga atgtgccact tggcagtgat 60

caccccataa ggattcaaac catgacgact tcagatacca aggatgttgc gaaaacagta 120

gaggaggtga tgaggatagc agataaagga gctgatcttg ttagaataac agtccagggt 180

aggaaggaag ctgatgcctg ctttgagatc aagaacactc tggttcagaa gaattacaac 240

attccactag tggccgatat tcattttgct cctacggtag ctctaagggt ggc 293

<210> 26
<211> 456
<212> DNA
<213> Zea mays

<400> 26

cagacaaggc ggaggaaaac tcgaactgtg atggtgggga atgtgccact tggcagtgat 60

caccccataa ggattcaaac catgacgact tcagatacca aggatgttgc gaaaacagta 120

gaggaggtga tgaggattgc agataaagga gctgatcttg ttagaataac agtccagggt 180

aggaaggaag ctgatgcctg ctttgagatc aagaacaact ctggttcaga agaattacaa 240

ccttccacta gtggacctga tattcatttt gctccttcag tagctttaaa ggtggcagaa 300

tgtttggaca aattaattga aacacacaat ttcttgttga tagtgtacct taattagaaa 360

agctggaatt taccggctac gacttccata aagcgcttgg gcttgtttaa caattggttt 420

ttaccttaat cgaatatttc acagaaattt gaattt 456

<210> 27
<211> 619
<212> DNA
<213> Zea mays

<400> 27

caccgaaggt ttctaattta tttctcagat ctcaataaat gtacaaaatg tgtagggatg 60

atgtacattg tatgctcagt tcctgcattg cgtgtttcgc tttacagaat atataaacta 120

cagacttggc tacagcctac agccctactc ctcggcagga ggatccaccc atcggccatg 180

gtccttgatc agctggatca aggcgtcagt tgcaccttcc atggcgatgg cgcgctgcac 240

aacggtcttg ccaacataaa ggtcgatctt tccgggagcg cctccaacgt atccgaaatc 300

ggcatcagcc atctctcctg gtccattgac aatacaaccc atgatagcga tcgaaacacc 360

tggcagatga gaggtctttt ctctaatctc agcgctgatt tcctgaaggt caaagagtgt 420

tcggccgcag gaaggacaag acacatattc agtttttgtg ttgcgcatcc tgcaaccttg 480

gagcaagttg aaagatgtgt ccctcaggaa ctcaaattcc tggtcagcag cttcaaggaa 540

tacaccatca ccaagaccat cgactaagag agcaccaacg ttggccccag caccaatgac 600

aagaccatct ctgtcaatg 619

<210> 28
<211> 422
<212> DNA
<213> Zea mays

<400> 28

tcgcttgcac ttgggtgtta cagaagctgg agagggtgaa gatggaagga tgaaatctgc 60

tattggcatt gggacactgc taatggatgg tttgggtgat acaatccgtg tctccctcac 120

agaaccacca gaagaagaga ttgatccttg ccaaaggttg gcaaatcttg ggacgcaggc 180

cgcaaacctt caaattgggg tggccccatt tgaagaaaag cacaggcgct attttgattt 240

ccagcgtagg agtggtcaat tgcctttgca gaaggaggga ggcgatagtt gactacagaa 300

atgtcctgca tcgtgatggt atctgactga tggcagtttc cctggatcag ttgaaggctc 360

ctgatctcct ttataggtat attgcagcaa agcttgcgga tggcatgcct ttcaaggatc 420

tg 422

<210> 29
<211> 430
<212> DNA
<213> Zea mays

<400> 29

tcgcttgcac ttgggtgtta cagaagctgg agagggtgaa gatggaagga tgaaatctgc 60

tattggcatt gggacactgc taatggatgg tttgggtgat acaatccgtg tctccctcac 120

agaaccacca gaagaagaga ttgatccttg ccaaaggttg gcaaatcttg ggacgcaggc 180

tgcaaacctt caaattgggg tggccccatt tgaagaaaag cacaggcgtt attttgattt 240

ccagcgtagg agtggtcaat tgcctttgca gaaggagggt gaggaagttg actacagaaa 300

tgtcctgcat cgtgatggta tctgtactga tggcagtttc cctggatcag ttgaaggctc 360

ctgatctcct ttataggtct cttgcagcaa agcttgcggt tggcatgcct ttcaaggatc 420

tggctactgt 430

<210> 30
<211> 528
<212> DNA
<213> Zea mays

<400> 30

gacaggcagg gtgcatgctg ctaggaggtt atttgagtac ttacaggcca atggcttgaa 60

cttccctgta attcatcaca taaatttccc tgaaaccatt gacagagatg gtcttgtcat 120

tggggctggg gccaacgttg gtgctctctt agtcgatggt cttggtgatg gtgtattcct 180

tgaggcggct gaccaggaat ttgagttcct gagggacaca tctttcaact tgctccaagg 240

ttgcaggatg cgcaacacaa aaactgaata tgtgtcttgt ccttcctgcg gccgaacact 300

ctttgacctt caggaaatca gcgctgagat tagcgaaaag acctctcatc tgccacgtgt 360

ttcgatcgct atcatgggtt gtattgtcaa tggaccagga gcgctggctg atgccgattt 420

cggatacgtt ggcggcgctc ccggaaagat cgacctttat attggcacga ccgttatgca 480

gcgcgccatc gccatggacg gtgcaactga cgccttgatc cagctgat 528

<210> 31
<211> 303
<212> DNA
<213> Zea mays

<400> 31

ggggccaacg ttggtgctct cttagtcgat ggtcttggtg atggtgtatt ccttgaggcg 60

gctgaccagg aatttgagtt cctgagggac acatctttca acttgctcca aggttgcagg 120

atgcgcaaca caaaaactga atatgtgtct tgtccttcct gcggccgaac actctttgac 180

cttcaggaaa tcagcgctga gattagagaa aagacctctc atctgccacg tgtttcgatc 240

gctatcatgg gttgtattgt caatggacca ggagagatgg ctgatgccga tttcggatac 300

gtt 303

<210> 32
<211> 613
<212> DNA
<213> Zea mays

<220>
<221> unsure
<222> (1..613)
<223> unsure at all n locations

<400> 32

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cttggaaaag ggagagaaac tcgcgcactc ggttatcgaa gggaggagcg cgggcgaggg 120

tgaggtttcg cccacacgga gctgcgaggt gtttgtagga tctcctaggt gagcccctgc 180

tgcttggaga cagccatggc caccggcgtg gctccagctc ctctcccaca tgtcagagtg 240

cgtcatgggg gcgtcgggtt caccaggagc gtcgattttg cgaaggtctt gtctgctccc 300

ggtgccggca cgatgagagc aagctcctct agaggcaggg cgctcgtggc gaagagctct 360

agtactggct cggagaccat ggagctcgag ccatcttcag aaggaagccc acttttagta 420

cccaggcaga agtactgtga atcaacacac cagacaagga ggaggaaaac tcgaactgtg 480

atggtgggga atgtgccact tggcagtgat catcccataa ggattcaaac catgacgact 540

tcagatacca aggatgttgc aaaaacagta gaggaggtga tgaggatagc agataaagga 600

gctgatcttg tta 613

<210> 33
<211> 464
<212> DNA
<213> Glycine max

<400> 33

agagcatgaa atcttctgcg aggaaaaggg tgtcaattat cacgaactca aatcctggcc 60

aagatattgc tgaacttcaa cctgcatccc caggaagccc tcttttggtt cctaggcaaa 120

agtattgtga atcattgcac aaacccatca ggagaaaaac aagcacagta atggttggta 180

acgtggctat tggtagcgag catcctataa gaattcagac catgactaca actgacacta 240

aggatgttgc tgggacagtt gaacaggtga tgagaatagc agataaagga gctgatattg 300

tacggataac agttcaaggg aagaaagaag ctgatgcttg ttttgagatt aaaaacaccc 360

ttgtgcagaa aaattacaac atacccgtgg tggctgatat tcattttgct ccctctgttg 420

ctttgcgggt agctgaatgc tttgataaga ttcgtgtaaa ccct 464

<210> 34
<211> 705
<212> DNA
<213> Glycine max

<400> 34

gtagctgaat gctttgataa gattcgtgta aaccctggaa attttgctga tagacgggct 60

caatttgaaa cattagagta cacagaagaa gactatcaga aagaacttga gcatattgaa 120

aaggttttca caccattggt tgagaaatgt aagaaatatg ggagagcaat gcgcattggg 180

acaaaccatg gaagtctttc tgatcgtata atgagctact atggagactc gcctagggga 240

atggtagaat ctgcttttga atttgcaagg atatgccgaa agttagacta tcacaatttt 300

gtttttttcta tgaaagcaag caacccagtt atcatggttc aggcataccg cttacttgtg 360

gctgaaatgt atgtccaagg ctgggattat ccattacact tgggtgttac tgaagctgga 420

gaaggtgagg atgggaggat gaagtctgca ataggcattg gaactcttct tcaggatgga 480

ttgggtgata caattagggt ttctctcaca gaaccaccag aggaggagat agacccttgc 540

agaaggttgg caaatcttgg aatgatagct tctgaactcc agaaggggtt ggaacctttt 600

gaagaaaagc acagacatta ttttcgactt tcagcgccga tctggtcaat tgccagtgca 660

aaaagagggt gaggaggtgg attacagagg tgtactgcac cgtga 705

<210> 35
<211> 564
<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (1..564)
<223> unsure at all n locations

<400> 35

aagcncggaa ttcggctcga gaggaactca aatcctggcc aagatattgc tgaacttcaa 60

cctgtatccc caggaagccc tcttttggtt cctaggcaaa agtattgtga atgattacac 120

aaaactgtca ggagaaaaac aaacacagtg atggttggta acgtggctat tggtagcgag 180

catcctataa gaattcagac catgactacg actgacacta aggatgttgc tgggacagtt 240

gaacaggtga tgagaatagc agataaagga gctgatattg tacggataac agttcaaggg 300

aagaaagaag ctgatgcttg ttttgagatt aaaaacaccc ttgttcagaa aaattacaac 360

atactcgtgg tggctgatat tcatttttgct ccctctggtg ctttgcgggt agctgaatgc 420

tttgataaga ttcgtgtaaa ccctggaaat tttgctgata gacgggctca atttgaaaca 480

ttagagtaca cagatgatga ctatcagaaa gaacttgagc atattgaaaa ggttttcaca 540

ccattggttg agaaatgtaa gaaa 564

<210> 36
<211> 511
<212> DNA
<213> Glycine max

<400> 36

aaaccatgga agtctttctg atcgtataat gagctactat ggagactcgc ctaggggaat 60

ggtagaatct gcttttgaat ttgcaaggat atgccgaaag ttagactatc acaattttgt 120

tttttctatg aaagcaagca acccagttat catggttcag gcataccgct tacttgtggc 180

tgaaatgtat gtccaaggct gggattatcc attacacttg ggtgttactg aagctggaga 240

aggtgaggat gggaggatga agtctgcaat aggcattgga actcttcttc aggatggatt 300

gggtgataca attagggttt ctctcacaga accaccagag gaggagatag acccttgcag 360

aaggttggca aatcttggaa tgatagcttc tgaactccag aaggggggtgg aacctttga 420

agaaaagcac agacattatt ttgactttca gcgccgatct ggtcaattgc cagtgcataa 480

agagggtgag gaggtggatt acagaggtgt a 511

<210> 37
<211> 498
<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (1..498)
<223> unsure at all n locations

<400> 37

cggaggtggc gtgaatgctt tgataagatt cgtgtaaacc ctggaaattt tgctgataga 60

cgggctcaat ttgaaacatg agagtggaca naataagact atgagaaaga acttgagcat 120

attgaaaagg ttttcacacc attggttgag aaatgtaaga aatatgggag agcaatgcgc 180

attgggacaa accatggaag tctttctgat cgtataatga gctactatgg agactcgcct 240

aggggaatgg tagaatctgc ttttgaattt gcaaggatat gccgaaagtt agactatcac 300

aattttgttt tttctatgaa agcaagcaac ccagttatca tggttcaggc ataccgctta 360

cttgtggctg aaatgtatgt ccaaggctgg gattatccat tacacttggg tgttactgaa 420

gctggagaag gtgaggatgg gaggatgaag tctgcaatag gcattggaac tcttcttcag 480

gatggattgg gtgataca 498

<210> 38
<211> 440
<212> DNA
<213> Glycine max

<400> 38

gtagctgaat gctttgataa gattcgtgta aaccctggaa attttgttga tagacgggct 60

caatttgaaa cattagagta cacagaagaa gactatcata aagaacttga gcatattgaa 120

aaggttttca caccattggt tgagaaatgt aagaaatatg ggagagcaat gcgcattggg 180

acaaaccatg gaagtctttc tgatcgtata atgagctact atggagactc gcctagggga 240

atggtagaat ctgcttttga atttgcaagg atatgccgaa agttagacta tcacaatttt 300

gtttttttcta tgaaagcaag caacccagtt atcatggttc aggcataccg cttacttgtg 360

gctgaaatgt atgttcaagg ctgggattat ccattacact tgggtgttac tgaagctgga 420

aaaagtgagg atgggaggat 440

<210> 39
<211> 353
<212> DNA
<213> Glycine max

<400> 39

aattcggctc gagaggaact caaatcctgg ccaagatatt gctgaacttc aacctgcatc 60

cccaggaagc cctcttttgg ttcctaggca aaagtattgt gaatcattac acaaaactgt 120

caggagaaaa acaaacacag tgatggttgg taacgtggct attggtagcg agcatcctat 180

aagaattcag accatgacta cgactgacac taaggatgtt gctgggacag ttgaacaggt 240

gatgagaata gcagataaag gagctgatat tgtacggata acagttcaag ggaagaaaga 300

agctgatgct tgttttgaga ttaaaaacac ccttgttcaa aaaaattaca aca 353

<210> 40
<211> 577
<212> DNA
<213> Glycine max

<400> 40

gatgtttttg tcgtgtattc tattcctatt gcattcagct cactgatttc aattacaaag 60

tcaattttgt aaatcagagg cagagagagt tgtaaagagc ctctgaattt tgatcacacc 120

acacccttct tctcatctcc accagaaatg gctaccggag ctgctgtgcc aactacgttt 180

tctaccctca agacatggga ttccagtttg gggtttgcaa aaaacataga ttttgtgaga 240

gtttccgata tgaagagcat gaaatcttct gcgaggaaaa gggtgtcaat tatcaggaac 300

tcaaatcctg gccaagatat tgctgaactt caacctgcat ccccaggaag ccctcttttg 360

gttcctaggc aaaagtattg tgaatcattg cacaaaccca tcaggagaaa aacaagcaca 420

gtaatggttg gtaacgtggc tattggtagc gagcatccta taagaattca gaccatgact 480

acaactgaca ctaaggatgt tgctgggaca gttgaaccgg tgatgagaat agcagataaa 540

ggagctgata ttgtacggat aacagttcaa gggaaga 577

<210> 41
<211> 551
<212> DNA
<213> Glycine max

<400> 41

tggtgctggt tctgatgctg gagcccttct ggtggatggg cttggagatg gacttctttt 60

ggaagcgcca gacaaggatt ttgaatttat tagaaacact tctttcaatt tgttgcaagg 120

ctgcagaatg agaaatacaa agacagagta tgtctcatgt ccatcctgtg gcagaacatt 180

gtttgatctt caagaagtaa gtgcacaaat tcgggagaag acatcacacc tccccggtgt 240

ttcgattgca atcatgggat gcattgtaaa tggaccaggg gagatggctg atgcagactt 300

tgggtatgtg ggaggcactc ccgggaagat tgacctctat gttgggaaga ctgtggtgaa 360

gcgtggaatt gcaatggagc atgcaaccaa tgccttgatc gatctaataa aagaacatgg 420

acgatgggtg gaccctcctg ccgaggagta aaagcaagag cttaattttg agattggcat 480

tcaaggccat agtaagatga gcattgtcat atccaattat tggacacatg taatataagc 540

atacactcaa t 551

<210> 42
<211> 869
<212> DNA
<213> Glycine max

<400> 42

gaagcatagt agcatcaatg ccttccttat acagaagact aaaattagca gagtgcatgc 60

ggccaggcgg ttatttgagt acctatccga caattctcta aacttccctg ttattcacca 120

tattcagttc ccaaatggga ttcacagaga tgacttggta attggtgctg gttctgatgc 180

tggagccctt ctggtggatg ggcttggaga tggacttctt ttggaagcgc cagacaagga 240

ttttgaattt attagaaaca cttctttcaa tttgttgcaa ggctgcagaa tgagaaatac 300

aaagacagag tatgtctcat gtccatcctg tggcagaaca ttgtttgatc ttcaagaagt 360

aagtgcacaa attcgggaga agacatcaca cctccctggt gtttcgattg caatcatggg 420

atgcattgta aatggaccag gggagatggc tgatgcagac tttgggtatg tgggaggcac 480

tcccgggaag attgacctct atgttgggaa gactgtggtg aagcgtggaa ttgcaatgga 540

gcatgcaacc aatgccttga tcgatctaat aaaagaacat ggacgatggg tggaccctcc 600

tgccgaggag taaaagcaag agcttaattt tgagattggc attcaaggcc atagtaagat 660

gagcattgtc atatccaatt attgtacaca tgtaatataa gataacactc aatgcttaag 720

tttgagccta gttttaagtt ccttttgaga aagatcccaa ttaaagcttg ttgtgaggaa 780

atcgacagct agaacatgta tacagataac agtgtattgc tttgccccat cagccatcaa 840

taataatgag aatctcttag aatagtgcc 869

<210> 43
<211> 291
<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (1..291)
<223> unsure at all n locations

<400> 43

gangnactca aatcctgggc caagatattg ctgaacttca nccctgcatc cccaggnngc 60

cctcttttgg ttcctaggca aaagtattgt gaatcattnc cacaaaactg nccagganaa 120

aaacaaacac agtgatggtt ggtaacgtgg ctattggtag cgagcatcct ataagaattc 180

agaccatgac tacgacngac actaaggatg ttgctgggac agtngaacng gtgatgagaa 240

tagcagataa aggagctgat attgtacgga taacagttca agggaagaaa g 291

<210> 44
<211> 388
<212> DNA
<213> Glycine max

<400> 44

cccggtatat ggttcaggca taccgtttac ttgtggctga aatgtatgtc caaggctggg 60

attatccatt acacttgggt gttactgaag ctggagaagg tgaggatggg aggatgaagt 120

ctgcaattgg cattggaact cttcttcagg atggattggg tgatacaatt agggtttctc 180

tcacagaacc accagaagag gagatagatc cttgcagaag gttggcaaat cttggaatga 240

gagcttctga actccagaag ggggtggaac cttttgaaga aaagcacaga cattattttg 300

acttccagcg ccgatctggt caattgccag tgcaaaaaga gggtgaggag gtggattaca 360

gaggtgcact gcaccgtgac ggttctgt 388

<210> 45
<211> 211
<212> DNA
<213> Glycine max

<400> 45

cccggttatc atggcgcagg cataccgctt acttgtggct gaaatgtatg tccaaggctg 60

ggattatcca ttacacttgg gtgttactga agctggagga ggtgaggatg acaggatgaa 120

gtctgcaatt ggcattggaa ctcttcttca ggatggattg ggtgatacaa ttagggtgtc 180

tcgcacagaa ccaccagaag aggagataga t 211

<210> 46
<211> 276
<212> DNA
<213> Glycine max

<400> 46

tgggcttgga gatggactac ttttggaagc cccggacaag gattttgaat ttattagaaa 60

cacttctttc aatttgttgc aaggctgcag aatgagaaat acaaagacag agtatgtctc 120

atgtccatcc tgtggcagaa cattgtttga tcttcaagaa gtaagtgcac aaattcggga 180

gaagacatca cacctccctg gtgtttcgat tgcaatcatg ggatgcattg taaatggacc 240

aggggagatg gctgatgcag actttgggta tgtggg 276

<210> 47
<211> 399
<212> DNA
<213> Brassica napus

<400> 47

cccacgcgtc cgcagggatt cacagggacg agttggtgat ccacgcaggg acatacgctg 60

gggcacttct agtggatgga cttggagatg gtgtaatgct agaagcacct gatcaagact 120

tcgagtttct taggaacact tctttcaact tgttacaagg ctgcaggatg cgtaacacca 180

agacggaata cgtatcgtgc ccgtcttgtg gaagaactct gttcgacttg caagaaatca 240

gcgctgagat cagagaaaag acttcgcatt tgcctggcgt ttcgattgca ataatgggtt 300

gcattgtgaa tggacctggc gaaatggctg atgctgattt cggttatgta ggcggttctc 360

ccgggaaaat cgacctttac gttggaaaga cggtggtca 399

<210> 48
<211> 740
<212> PRT
<213> Arabidopsis thaliana

<400> 48

Met Ala Thr Gly Val Leu Pro Ala Pro Val Ser Gly Ile Lys Ile Pro
1 5 10 15

Asp Ser Lys Val Gly Phe Gly Lys Ser Met Asn Leu Val Arg Ile Cys
20 25 30

Asp Val Arg Ser Leu Arg Ser Ala Arg Arg Arg Val Ser Val Ile Arg
35 40 45

Asn Ser Asn Gln Gly Ser Asp Leu Ala Glu Leu Gln Pro Ala Ser Glu
50 55 60

Gly Ser Pro Leu Leu Val Pro Arg Gln Lys Tyr Cys Glu Ser Leu His
65 70 75 80

Lys Thr Val Arg Arg Lys Thr Arg Thr Val Met Val Gly Asn Val Ala
85 90 95

Leu Gly Ser Glu His Pro Ile Arg Ile Gln Thr Met Thr Thr Ser Asp
100 105 110

Thr Lys Asp Ile Thr Gly Thr Val Asp Glu Val Met Arg Ile Ala Asp
115 120 125

Lys Gly Ala Asp Ile Val Arg Ile Thr Val Gln Gly Lys Lys Glu Ala
130 135 140

Asp Ala Cys Phe Glu Ile Lys Asp Lys Leu Val Gln Leu Asn Tyr Asn
145 150 155 160

Ile Pro Leu Val Ala Asp Ile His Phe Ala Pro Thr Val Ala Leu Arg
165 170 175

Val Ala Glu Cys Phe Asp Lys Ile Arg Val Asn Pro Gly Asn Phe Ala
180 185 190

Asp Arg Arg Ala Gln Phe Glu Thr Ile Asp Tyr Thr Glu Asp Glu Tyr
195 200 205

Gln Lys Glu Leu Gln His Ile Glu Gln Val Phe Thr Pro Leu Val Glu
210 215 220

Lys Cys Lys Lys Tyr Gly Arg Ala Met Arg Ile Gly Thr Asn His Gly
225 230 235 240

Ser Leu Ser Asp Arg Ile Met Ser Tyr Tyr Gly Asp Ser Pro Arg Gly
245 250 255

Met Val Glu Ser Ala Phe Glu Phe Ala Arg Ile Cys Arg Lys Leu Asp
260 265 270

Tyr His Asn Phe Val Phe Ser Met Lys Ala Ser Asn Pro Val Ile Met
275 280 285

Val Gln Ala Tyr Arg Leu Leu Val Ala Glu Met Tyr Val His Gly Trp
290 295 300

Asp Tyr Pro Leu His Leu Gly Val Thr Glu Ala Gly Glu Gly Glu Asp
305 310 315 320

Gly Arg Met Lys Ser Ala Ile Gly Ile Gly Thr Leu Leu Gln Asp Gly
325 330 335

Leu Gly Asp Thr Ile Arg Val Ser Leu Thr Glu Pro Pro Glu Glu Glu
340 345 350

Ile Asp Pro Cys Arg Arg Leu Ala Asn Leu Gly Thr Lys Ala Ala Lys
355 360 365

Leu Gln Gln Gly Ala Pro Phe Glu Glu Lys His Arg His Tyr Phe Asp
370 375 380

Phe Gln Arg Arg Thr Gly Asp Leu Pro Val Gln Lys Glu Gly Glu Glu
385 390 395 400

Val Asp Tyr Arg Asn Val Leu His Arg Asp Gly Ser Val Leu Met Ser
405 410 415

Ile Ser Leu Asp Gln Leu Lys Ala Pro Glu Leu Leu Tyr Arg Ser Leu
420 425 430

Ala Thr Lys Leu Val Val Gly Met Pro Phe Lys Asp Leu Ala Thr Val
435 440 445

Asp Ser Ile Leu Leu Arg Glu Leu Pro Pro Val Asp Asp Gln Val Ala
450 455 460

Arg Leu Ala Leu Lys Arg Leu Ile Asp Val Ser Met Gly Val Ile Ala
465 470 475 480

Pro Leu Ser Glu Gln Leu Thr Lys Pro Leu Pro Asn Ala Met Val Leu
485 490 495

Val Asn Leu Lys Glu Leu Ser Gly Gly Ala Tyr Lys Leu Leu Pro Glu
500 505 510

Gly Thr Arg Leu Val Val Ser Leu Arg Gly Asp Glu Pro Tyr Glu Glu
515 520 525

Leu Glu Ile Leu Lys Asn Ile Asp Ala Thr Met Ile Leu His Asp Val
530 535 540

Pro Phe Thr Glu Asp Lys Val Ser Arg Val His Ala Ala Arg Arg Leu
545 550 555 560

Phe Glu Phe Leu Ser Glu Asn Ser Val Asn Phe Pro Val Ile His His
565 570 575

Ile Asn Phe Pro Thr Gly Ile His Arg Asp Glu Leu Val Ile His Ala
580 585 590

Gly Thr Tyr Ala Gly Gly Leu Leu Val Asp Gly Leu Gly Asp Gly Val
595 600 605

Met Leu Glu Ala Pro Asp Gln Asp Phe Asp Phe Leu Arg Asn Thr Ser
610 615 620

Phe Asn Leu Leu Gln Gly Cys Arg Met Arg Asn Thr Lys Thr Glu Tyr
625 630 635 640

```
Val Ser Cys Pro Ser Cys Gly Arg Thr Leu Phe Asp Leu Gln Glu Ile
                645                 650                 655

Ser Ala Glu Ile Arg Glu Lys Thr Ser His Leu Pro Gly Val Ser Ile
            660                 665                 670

Ala Ile Met Gly Cys Ile Val Asn Gly Pro Gly Glu Met Ala Asp Ala
        675                 680                 685

Asp Phe Gly Tyr Val Gly Gly Ser Pro Gly Lys Ile Asp Leu Tyr Val
    690                 695                 700

Gly Lys Thr Val Val Lys Arg Gly Ile Ala Met Thr Glu Ala Thr Asp
705                 710                 715                 720

Ala Leu Ile Gly Leu Ile Lys Glu His Gly Arg Trp Val Asp Pro Pro
                725                 730                 735

Val Ala Asp Glu
            740
```

<210> 49
<211> 603
<212> PRT
<213> Oryza sativa

<400> 49

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Met Val Gly Asn Val Pro Leu Gly Ser Asp His Pro Ile Arg Ile Gln
1               5                   10                  15

Thr Met Thr Thr Ser Asp Thr Lys Asp Val Ala Lys Thr Val Glu Glu
            20                  25                  30

Val Met Arg Ile Ala Asp Lys Gly Ala Asp Phe Val Arg Ile Thr Val
        35                  40                  45

Gln Gly Arg Lys Glu Ala Asp Ala Cys Phe Glu Ile Lys Asn Thr Leu
    50                  55                  60

Val Gln Lys Asn Tyr Asn Ile Pro Leu Val Ala Asp Ile His Phe Ala
65                  70                  75                  80

Pro Thr Val Ala Leu Arg Val Ala Glu Cys Phe Asp Lys Ile Arg Val
                85                  90                  95

Asn Pro Gly Asn Phe Ala Asp Arg Arg Ala Gln Phe Glu Gln Leu Glu
            100                 105                 110

Tyr Thr Glu Asp Asp Tyr Gln Lys Glu Leu Glu His Ile Glu Lys Val
        115                 120                 125

Pro Asn Ile Ser Leu Phe Ser Val Asn Leu Val Phe Ser Pro Leu Val
    130                 135                 140
```

```
Glu Lys Cys Lys Gln Tyr Gly Arg Ala Met Arg Ile Gly Thr Asn His
145                 150                 155                 160

Gly Ser Leu Ser Asp Arg Ile Met Ser Tyr Tyr Gly Asp Ser Pro Arg
                165                 170                 175

Gly Met Val Glu Ser Ala Leu Glu Phe Ala Arg Ile Cys Arg Lys Leu
            180                 185                 190

Asp Phe His Asn Phe Val Phe Ser Met Lys Ala Ser Asn Pro Val Ile
        195                 200                 205

Met Val Gln Ala Tyr Arg Leu Leu Val Ala Glu Met Tyr Asn Leu Gly
    210                 215                 220

Trp Asp Tyr Pro Leu His Leu Gly Val Thr Glu Ala Gly Glu Gly Glu
225                 230                 235                 240

Asp Gly Arg Met Lys Ser Ala Ile Gly Ile Gly Thr Leu Leu Met Asp
                245                 250                 255

Gly Leu Gly Asp Thr Ile Arg Val Ser Leu Thr Glu Pro Pro Glu Glu
            260                 265                 270

Glu Ile Asp Pro Cys Arg Arg Leu Ala Asn Leu Gly Thr His Ala Ala
        275                 280                 285

Asp Leu Gln Ile Gly Val Ala Pro Phe Glu Glu Lys His Arg Arg Tyr
    290                 295                 300

Phe Asp Phe Gln Arg Arg Ser Gly Gln Leu Pro Leu Gln Lys Glu Ala
305                 310                 315                 320

Pro Glu Leu Leu Tyr Arg Ser Leu Ala Ala Lys Leu Val Val Gly Met
                325                 330                 335

Pro Phe Lys Asp Leu Ala Thr Val Asp Ser Ile Leu Leu Lys Glu Leu
            340                 345                 350

Pro Pro Val Glu Asp Ala Gln Ala Arg Leu Ala Leu Lys Arg Leu Val
        355                 360                 365

Asp Ile Ser Met Gly Val Leu Thr Pro Leu Ser Glu Gln Leu Thr Lys
    370                 375                 380

Pro Leu Pro His Ala Ile Ala Leu Val Asn Val Asp Glu Leu Ser Ser
385                 390                 395                 400

Gly Ala His Lys Leu Leu Pro Glu Gly Thr Arg Leu Ala Val Thr Leu
                405                 410                 415

Arg Gly Asp Glu Ser Tyr Glu Gln Leu Asp Leu Leu Lys Gly Val Asp
            420                 425                 430

Asp Ile Thr Met Leu Leu His Ser Val Pro Tyr Gly Glu Glu Lys Thr
        435                 440                 445
```

Gly Arg Val His Ala Ala Arg Arg Leu Phe Glu Tyr Leu Glu Thr Asn
450 455 460

Gly Leu Asn Phe Pro Val Ile His His Ile Glu Phe Pro Lys Ser Val
465 470 475 480

Asn Arg Asp Asp Leu Val Ile Gly Ala Gly Ala Asn Val Gly Ala Leu
485 490 495

Leu Val Asp Gly Leu Gly Asp Gly Val Leu Leu Glu Ala Ala Asp Gln
500 505 510

Glu Phe Glu Phe Leu Arg Asp Thr Ser Phe Asn Leu Leu Gln Gly Cys
515 520 525

Arg Met Arg Asn Thr Lys Thr Ile Ala Ile Met Gly Cys Ile Val Asn
530 535 540

Gly Pro Gly Glu Met Ala Asp Ala Asp Phe Gly Tyr Val Gly Gly Ala
545 550 555 560

Pro Gly Lys Ile Asp Leu Tyr Val Gly Lys Thr Val Val Gln Arg Gly
565 570 575

Ile Ala Met Glu Gly Ala Thr Asp Ala Leu Ile Gln Leu Ile Lys Asp
580 585 590

His Gly Arg Trp Val Asp Pro Pro Val Glu Glu
595 600

<210> 50
<211> 372
<212> PRT
<213> Escherichia coli

<400> 50

Met His Asn Gln Ala Pro Ile Gln Arg Arg Lys Ser Thr Arg Ile Tyr
1 5 10 15

Val Gly Asn Val Pro Ile Gly Asp Gly Ala Pro Ile Ala Val Gln Ser
20 25 30

Met Thr Asn Thr Arg Thr Thr Asp Val Glu Ala Thr Val Asn Gln Ile
35 40 45

Lys Ala Leu Glu Arg Val Gly Ala Asp Ile Val Arg Val Ser Val Pro
50 55 60

Thr Met Asp Ala Ala Glu Ala Phe Lys Leu Ile Lys Gln Gln Val Asn
65 70 75 80

Val Pro Leu Val Ala Asp Ile His Phe Asp Tyr Arg Ile Ala Leu Lys
85 90 95

Val Ala Glu Tyr Gly Val Asp Cys Leu Arg Ile Asn Pro Gly Asn Ile
100 105 110

Gly Asn Glu Glu Arg Ile Arg Met Val Val Asp Cys Ala Arg Asp Lys
115 120 125

Asn Ile Pro Ile Arg Ile Gly Val Asn Ala Gly Ser Leu Glu Lys Asp
130 135 140

Leu Gln Glu Lys Tyr Gly Glu Pro Thr Pro Gln Ala Leu Leu Glu Ser
145 150 155 160

Ala Met Arg His Val Asp His Leu Asp Arg Leu Asn Phe Asp Gln Phe
165 170 175

Lys Val Ser Val Lys Ala Ser Asp Val Phe Leu Ala Val Glu Ser Tyr
180 185 190

Arg Leu Leu Ala Lys Gln Ile Asp Gln Pro Leu His Leu Gly Ile Thr
195 200 205

Glu Ala Gly Gly Ala Arg Ser Gly Ala Val Lys Ser Ala Ile Gly Leu
210 215 220

Gly Leu Leu Leu Ser Glu Gly Ile Gly Asp Thr Leu Arg Val Ser Leu
225 230 235 240

Ala Ala Asp Pro Val Glu Glu Ile Lys Val Gly Phe Asp Ile Leu Lys
245 250 255

Ser Leu Arg Ile Arg Ser Arg Gly Ile Asn Phe Ile Ala Cys Pro Thr
260 265 270

Cys Ser Arg Gln Glu Phe Asp Val Ile Gly Thr Val Asn Ala Leu Glu
275 280 285

Gln Arg Leu Glu Asp Ile Ile Thr Pro Met Asp Val Ser Ile Ile Gly
290 295 300

Cys Val Val Asn Gly Pro Gly Glu Ala Leu Val Ser Thr Leu Gly Val
305 310 315 320

Thr Gly Gly Asn Lys Lys Ser Gly Leu Tyr Glu Asp Gly Val Arg Lys
325 330 335

Asp Arg Leu Asp Asn Asn Asp Met Ile Asp Gln Leu Glu Ala Arg Ile
340 345 350

Arg Ala Lys Ala Ser Gln Leu Asp Glu Ala Arg Arg Ile Asp Val Gln
355 360 365

Gln Val Glu Lys
370

<210> 51
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed primer named CINCO

<400> 51

cgctgcccag aatggacctc cctag 25

<210> 52
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed primer named SEIS

<400> 52

cagccgcgtt ttgacttgaa acgtgc 26

<210> 53
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed primer named MPD-Nde5'

<400> 53

gccatatgac cgtttacaca gcatccg 27

<210> 54
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed primer named MPD-Eco3'

<400> 54

tcgaattctc attattcctt tggtagacca gtctt 35

<210> 55
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed primer named hPMK1

<400> 55

tggttaacat atggccccgc tgggaggcgc 30

<210> 56
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed primer named hPMK4

<400> 56

aggttaactc aattaaagtc tggagcggat aaattctatc 40

<210> 57
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed primer named UNO

<400> 57

cgggcctcgt ttggctgtcg cactg 25

<210> 58
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed primer named DOS

<400> 58

cgcgggtgga aggaccttgt ggagg 25

<210> 59
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed primer named MK-Hpa5'

<400> 59

aagttaacat atgtcattac cgttcttaac ttc 33

<210> 60
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed primer named MK-Hpa3'

<400> 60

cggttaactc attatgaagt ccatggtaaa ttcg 34

<210> 61
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed primer named idi5X

<400> 61

cccctcgaga ttatgcaaac ggaacacgtc 30

<210> 62
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed primer named idi3X

<400> 62

ggctcgagtt atttaagctg ggtaaatgca g 31

<210> 63
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed primer named pBAD-mut1

<400> 63

ctgagagtgc accatctgcg gtgtgaaata cc 32

<210> 64
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed primer named pBAD-Link1

<400> 64

aattctaagg aggtttaaac taaggaggta cgtaaggagg 40

<210> 65
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed primer named pBAD-Link2

<400> 65

tcgacctcct tacgtacctc cttagtttaa acctccttag 40

<210> 66
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed primer named pBAD-D2

<400> 66

tcatactccc gccattcaga g 21

<210> 67
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed primer named pBAD-U3

<400> 67

ccgccaaaac agccaagctt g 21

<210> 68
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed primer named pRS-L1

<400> 68

gatccgttta aacgcccggg cggccgcg 28

<210> 69
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed primer named pRS-L2

<400> 69

aattcgcggc cgcccgggcg tttaaacg 28

<210> 70
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed primer named 1PE

<400> 70

cgcggtgtgg gtgagcatga tg 22

<210> 71
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed primer named 22PE

<400> 71

aaatctcccg ggttacccgt ctgttactgc 30

<210> 72
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed primer named 3PE

<400> 72

gcgtttaaac tggacgaagc gcgtcgaatt gac 33

<210> 73
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed primer named 4PE

<400> 73

tgcacgaccg cccagttgtt cc 22

<210> 74
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed primer named CAT1

<400> 74

gagtccgaat aaatacctgt g 21

<210> 75
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed primer named CAT4

<400> 75

ccgaatttct gccattcatc c 21

<210> 76
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed primer named 0PE

<400> 76

tgggctttgt cacgagcaca c 21

<210> 77
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed primer named 5PE

<400> 77

ggcccatagc aaaaccgaca g 21

<210> 78
<211> 372
<212> PRT
<213> Escherichia coli

<400> 78

Met His Asn Gln Ala Pro Ile Gln Arg Arg Lys Ser Thr Arg Ile Tyr
1 5 10 15

Val Gly Asn Val Pro Ile Gly Asp Gly Ala Pro Ile Ala Val Gln Ser
20 25 30

Met Thr Asn Thr Arg Thr Thr Asp Val Glu Ala Thr Val Asn Gln Ile
35 40 45

Lys Ala Leu Glu Arg Val Gly Ala Asp Ile Val Arg Val Ser Val Pro
50 55 60

Thr Met Asp Ala Ala Glu Ala Phe Lys Leu Ile Lys Gln Gln Val Asn
65 70 75 80

```
Val Pro Leu Val Ala Asp Ile His Phe Asp Tyr Arg Ile Ala Leu Lys
                85                  90                  95

Val Ala Glu Tyr Gly Val Asp Cys Leu Arg Ile Asn Pro Gly Asn Ile
            100                 105                 110

Gly Asn Glu Glu Arg Ile Arg Met Val Val Asp Cys Ala Arg Asp Lys
        115                 120                 125

Asn Ile Pro Ile Arg Ile Gly Val Asn Ala Gly Ser Leu Glu Lys Asp
    130                 135                 140

Leu Gln Glu Lys Tyr Gly Glu Pro Thr Pro Gln Ala Leu Leu Glu Ser
145                 150                 155                 160

Ala Met Arg His Val Asp His Leu Asp Arg Leu Asn Phe Asp Gln Phe
                165                 170                 175

Lys Val Ser Val Lys Ala Ser Asp Val Phe Leu Ala Val Glu Ser Tyr
            180                 185                 190

Arg Leu Leu Ala Lys Gln Ile Asp Gln Pro Leu His Leu Gly Ile Thr
        195                 200                 205

Glu Ala Gly Gly Ala Arg Ser Gly Ala Val Lys Ser Ala Ile Gly Leu
    210                 215                 220

Gly Leu Leu Leu Ser Glu Gly Ile Gly Asp Thr Leu Arg Val Ser Leu
225                 230                 235                 240

Ala Ala Asp Pro Val Glu Glu Ile Lys Val Gly Phe Asp Ile Leu Lys
                245                 250                 255

Ser Leu Arg Ile Arg Ser Arg Gly Ile Asn Phe Ile Ala Cys Pro Thr
            260                 265                 270

Cys Ser Arg Gln Glu Phe Asp Val Ile Gly Thr Val Asn Ala Leu Glu
        275                 280                 285

Gln Arg Leu Glu Asp Ile Ile Thr Pro Met Asp Val Ser Ile Ile Gly
    290                 295                 300

Cys Val Val Asn Gly Pro Gly Glu Ala Leu Val Ser Thr Leu Gly Val
305                 310                 315                 320

Thr Gly Gly Asn Lys Lys Ser Gly Leu Tyr Glu Asp Gly Val Arg Lys
                325                 330                 335

Asp Arg Leu Asp Asn Asn Asp Met Ile Asp Gln Leu Glu Ala Arg Ile
            340                 345                 350

Arg Ala Lys Ala Ser Gln Leu Asp Glu Ala Arg Arg Ile Asp Val Gln
        355                 360                 365

Gln Val Glu Lys
    370
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<210> 79
<211> 740
<212> PRT
<213> Arabidopsis thaliana

<400> 79

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Met Ala Thr Gly Val Leu Pro Ala Pro Val Ser Gly Ile Lys Ile Pro
1               5                  10                  15

Asp Ser Lys Val Gly Phe Gly Lys Ser Met Asn Leu Val Arg Ile Cys
            20                  25                  30

Asp Val Arg Ser Leu Arg Ser Ala Arg Arg Arg Val Ser Val Ile Arg
        35                  40                  45

Asn Ser Asn Gln Gly Ser Asp Leu Ala Glu Leu Gln Pro Ala Ser Glu
    50                  55                  60

Gly Ser Pro Leu Leu Val Pro Arg Gln Lys Tyr Cys Glu Ser Leu His
65                  70                  75                  80

Lys Thr Val Arg Arg Lys Thr Arg Thr Val Met Val Gly Asn Val Ala
                85                  90                  95

Leu Gly Ser Glu His Pro Ile Arg Ile Gln Thr Met Thr Thr Ser Asp
            100                 105                 110

Thr Lys Asp Ile Thr Gly Thr Val Asp Glu Val Met Arg Ile Ala Asp
        115                 120                 125

Lys Gly Ala Asp Ile Val Arg Ile Thr Val Gln Gly Lys Lys Glu Ala
    130                 135                 140

Asp Ala Cys Phe Glu Ile Lys Asp Lys Leu Val Gln Leu Asn Tyr Asn
145                 150                 155                 160

Ile Pro Leu Val Ala Asp Ile His Phe Ala Pro Thr Val Ala Leu Arg
                165                 170                 175

Val Ala Glu Cys Phe Asp Lys Ile Arg Val Asn Pro Gly Asn Phe Ala
            180                 185                 190

Asp Arg Arg Ala Gln Phe Glu Thr Ile Asp Tyr Thr Glu Asp Glu Tyr
        195                 200                 205

Gln Lys Glu Leu Gln His Ile Glu Gln Val Phe Thr Pro Leu Val Glu
    210                 215                 220

Lys Cys Lys Lys Tyr Gly Arg Ala Met Arg Ile Gly Thr Asn His Gly
225                 230                 235                 240

Ser Leu Ser Asp Arg Ile Met Ser Tyr Tyr Gly Asp Ser Pro Arg Gly
                245                 250                 255
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Met Val Glu Ser Ala Phe Glu Phe Ala Arg Ile Cys Arg Lys Leu Asp
260 265 270

Tyr His Asn Phe Val Phe Ser Met Lys Ala Ser Asn Pro Val Ile Met
275 280 285

Val Gln Ala Tyr Arg Leu Leu Val Ala Glu Met Tyr Val His Gly Trp
290 295 300

Asp Tyr Pro Leu His Leu Gly Val Thr Glu Ala Gly Glu Gly Glu Asp
305 310 315 320

Gly Arg Met Lys Ser Ala Ile Gly Ile Gly Thr Leu Leu Gln Asp Gly
325 330 335

Leu Gly Asp Thr Ile Arg Val Ser Leu Thr Glu Pro Pro Glu Glu Glu
340 345 350

Ile Asp Pro Cys Arg Arg Leu Ala Asn Leu Gly Thr Lys Ala Ala Lys
355 360 365

Leu Gln Gln Gly Ala Pro Phe Glu Glu Lys His Arg His Tyr Phe Asp
370 375 380

Phe Gln Arg Arg Thr Gly Asp Leu Pro Val Gln Lys Glu Gly Glu Glu
385 390 395 400

Val Asp Tyr Arg Asn Val Leu His Arg Asp Gly Ser Val Leu Met Ser
405 410 415

Ile Ser Leu Asp Gln Leu Lys Ala Pro Glu Leu Leu Tyr Arg Ser Leu
420 425 430

Ala Thr Lys Leu Val Val Gly Met Pro Phe Lys Asp Leu Ala Thr Val
435 440 445

Asp Ser Ile Leu Leu Arg Glu Leu Pro Pro Val Asp Asp Gln Val Ala
450 455 460

Arg Leu Ala Leu Lys Arg Leu Ile Asp Val Ser Met Gly Val Ile Ala
465 470 475 480

Pro Leu Ser Glu Gln Leu Thr Lys Pro Leu Pro Asn Ala Met Val Leu
485 490 495

Val Asn Leu Lys Glu Leu Ser Gly Gly Ala Tyr Lys Leu Leu Pro Glu
500 505 510

Gly Thr Arg Leu Val Val Ser Leu Arg Gly Asp Glu Pro Tyr Glu Glu
515 520 525

Leu Glu Ile Leu Lys Asn Ile Asp Ala Thr Met Ile Leu His Asp Val
530 535 540

Pro Phe Thr Glu Asp Lys Val Ser Arg Val His Ala Ala Arg Arg Leu
545 550 555 560

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Phe Glu Phe Leu Ser Glu Asn Ser Val Asn Phe Pro Val Ile His His
                565                 570                 575

Ile Asn Phe Pro Thr Gly Ile His Arg Asp Glu Leu Val Ile His Ala
            580                 585                 590

Gly Thr Tyr Ala Gly Gly Leu Leu Val Asp Gly Leu Gly Asp Gly Val
        595                 600                 605

Met Leu Glu Ala Pro Asp Gln Asp Phe Asp Phe Leu Arg Asn Thr Ser
    610                 615                 620

Phe Asn Leu Leu Gln Gly Cys Arg Met Arg Asn Thr Lys Thr Glu Tyr
625                 630                 635                 640

Val Ser Cys Pro Ser Cys Gly Arg Thr Leu Phe Asp Leu Gln Glu Ile
                645                 650                 655

Ser Ala Glu Ile Arg Glu Lys Thr Ser His Leu Pro Gly Val Ser Ile
            660                 665                 670

Ala Ile Met Gly Cys Ile Val Asn Gly Pro Gly Glu Met Ala Asp Ala
        675                 680                 685

Asp Phe Gly Tyr Val Gly Gly Ser Pro Gly Lys Ile Asp Leu Tyr Val
    690                 695                 700

Gly Lys Thr Val Val Lys Arg Gly Ile Ala Met Thr Glu Ala Thr Asp
705                 710                 715                 720

Ala Leu Ile Gly Leu Ile Lys Glu His Gly Arg Trp Val Asp Pro Pro
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Val Ala Asp Glu
            740
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<211> 155
<212> DNA
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<400> 80

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ggattcgaaa gtcgggtttg gtaaaagcat gaatcttgtg agaatttgtg atgttaggag  120
tctaagatct gctgatgagt agatttcata aaagt                             155
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Asp Ser Lys Val Gly Phe Gly Lys Ser Met Asn Leu Val Arg Ile Cys
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Asp Val Arg Ser Leu Arg Ser Ala Asp Glu
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<210> 83
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<400> 83

Met Arg Gly Ser His His His His His His Gly Ser
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<211> 59
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<400> 84
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Met Arg Gly Ser His His His His His His Gly Ser Ala Asp Glu
1 5 10 15